

2012-2014 citations of the three main VISTA papers:

(Mayor et al., Bioinformatics. 2000 Nov;16(11):1046-7; Loots et al., Genome Res. 2002 May;12(5):832-9; Frazer et al., Nucleic Acids Res. 2004 Jul 1;32(Web Server issue):W273-9)

1. Alexander, M.R., et al., *Interleukin-1 beta modulates smooth muscle cell phenotype to a distinct inflammatory state relative to PDGF-DD via NF-kappa B-dependent mechanisms*. Physiological Genomics, 2012. **44**(7): p. 417-429.
2. Altmann, A., et al., *A beginners guide to SNP calling from high-throughput DNA-sequencing data*. Human Genetics, 2012. **131**(10): p. 1541-1554.
3. Ariza-Cosano, A., et al., *Differences in enhancer activity in mouse and zebrafish reporter assays are often associated with changes in gene expression*. Bmc Genomics, 2012. **13**.
4. Bei, L., et al., *beta-Catenin Activates the HOXA10 and CDX4 Genes in Myeloid Progenitor Cells*. Journal of Biological Chemistry, 2012. **287**(47).
5. Bei, L., et al., *beta-Catenin Activates the HOXA10 and CDX4 Genes in Myeloid Progenitor Cells*. Journal of Biological Chemistry, 2012. **287**(47).
6. Brasil, A.S., et al., *KRAS gene mutations in Noonan syndrome familial cases cluster in the vicinity of the switch II region of the G-domain: Report of another family with metopic cranosynostosis*. American Journal of Medical Genetics Part A, 2012. **158A**(5): p. 1178-1184.
7. Breuninger, H. and M. Lenhard, *Expression of the central growth regulator BIG BROTHERR is regulated by multiple cis-elements*. Bmc Plant Biology, 2012. **12**.
8. Butchar, J.P., et al., *New Negative Feedback Regulators of Egfr Signaling in Drosophila*. Genetics, 2012. **191**(4): p. 1213-U260.
9. Camp, J.G., et al., *Intronic Cis-Regulatory Modules Mediate Tissue-Specific and Microbial Control of angptl4/flaf Transcription*. Plos Genetics, 2012. **8**(3).
10. Capriotti, E., et al., *Bioinformatics for personal genome interpretation*. Briefings in Bioinformatics, 2012. **13**(4): p. 495-512.
11. Chatterjee, M., et al., *Gbx2 regulates thalamocortical axon guidance by modifying the LIM and Robo codes*. Development, 2012. **139**(24): p. 4633-4643.
12. Chauhan, S., et al., *Evolution of the Cdk-activator Speedy/RINGO in vertebrates*. Cellular and Molecular Life Sciences, 2012. **69**(22): p. 3835-3850.
13. Chen, R., et al., *Genome-wide analysis and environmental response profiling of SOT family genes in rice (*Oryza sativa*)*. Genes & Genomics, 2012. **34**(5): p. 549-560.
14. Crow, K.D., et al., *An Independent Genome Duplication Inferred from Hox Paralogs in the American Paddlefish-A Representative Basal Ray-Finned Fish and Important Comparative Reference*. Genome Biology and Evolution, 2012. **4**(9): p. 937-953.
15. Cutty, S.J., et al., *Identification and expression analysis of two novel members of the Mesp family in zebrafish*. International Journal of Developmental Biology, 2012. **56**(4): p. 285-294.
16. Das, A. and J.G. Crump, *Bmps and Id2a Act Upstream of Twist1 To Restrict*

- Ectomesenchyme Potential of the Cranial Neural Crest.* Plos Genetics, 2012. **8**(5).
- 17. del Blanco, B., et al., *Tcra Enhancer Activation by Inducible Transcription Factors Downstream of Pre-TCR Signaling.* Journal of Immunology, 2012. **188**(7): p. 3278-3293.
  - 18. Dewey, C.N., *Whole-Genome Alignment*, in *Evolutionary Genomics: Statistical and Computational Methods*, Vol 1, M. Anisimova, Editor. 2012. p. 237-257.
  - 19. Diallo, A.O., et al., *Expression of vernalization responsive genes in wheat is associated with histone H3 trimethylation.* Molecular Genetics and Genomics, 2012. **287**(7): p. 575-590.
  - 20. Eldarov, M.A., et al., *Complete mitochondrial genome of compactin-producing fungus Penicillium solitum and comparative analysis of Trichocomaceae mitochondrial genomes.* Fems Microbiology Letters, 2012. **329**(1): p. 9-17.
  - 21. Elrouby, N. and T.E. Bureau, *Modulation of AUXIN-BINDING PROTEIN 1 gene expression in maize and the teosintes by transposon insertions in its promoter.* Molecular Genetics and Genomics, 2012. **287**(2): p. 143-153.
  - 22. Faure, S., et al., *Mutation at the circadian clock gene EARLY MATURITY 8 adapts domesticated barley (*Hordeum vulgare*) to short growing seasons.* Proceedings of the National Academy of Sciences of the United States of America, 2012. **109**(21): p. 8328-8333.
  - 23. Feltus, F.A. and J.P. Vandenbrink, *Bioenergy grass feedstock: current options and prospects for trait improvement using emerging genetic, genomic, and systems biology toolkits.* Biotechnology for Biofuels, 2012. **5**.
  - 24. Fernandez-Suarez, X.M., *Analyzing genomic data: understanding the genome.* Wiley Interdisciplinary Reviews-Data Mining and Knowledge Discovery, 2012. **2**(2): p. 116-137.
  - 25. Ford, B.A., J.R. Ernest, and A.R. Gendall, *Identification and characterization of orthologs of AtNHX5 and AtNHX6 in Brassica napus.* Frontiers in Plant Science, 2012. **3**.
  - 26. Fujito, N.T. and M. Nonaka, *Highly divergent dimorphic alleles of the proteasome subunit beta type-8 (PSMB8) gene of the bichir *Polypterus senegalus*: implication for evolution of the PSMB8 gene of jawed vertebrates.* Immunogenetics, 2012. **64**(6): p. 447-453.
  - 27. Garnett, A.T., T.A. Square, and D.M. Medeiros, *BMP, Wnt and FGF signals are integrated through evolutionarily conserved enhancers to achieve robust expression of Pax3 and Zic genes at the zebrafish neural plate border.* Development, 2012. **139**(22): p. 4220-4231.
  - 28. Gautam, N., et al., *Genome-wide identification of rice class I metallothionein gene: tissue expression patterns and induction in response to heavy metal stress.* Functional & Integrative Genomics, 2012. **12**(4): p. 635-647.
  - 29. Gleixner, E., et al., *Testes-specific hemoglobins in *Drosophila* evolved by a combination of sub- and neofunctionalization after gene duplication.* Bmc Evolutionary Biology, 2012. **12**.
  - 30. Godi, M., et al., *Functional SNPs within the Intron 1 of the PROP1 Gene Contribute to Combined Growth Hormone Deficiency (CPHD).* Journal of Clinical Endocrinology & Metabolism, 2012. **97**(9): p. E1791-E1797.

31. Goodstein, D.M., et al., *Phytozome: a comparative platform for green plant genomics*. Nucleic Acids Research, 2012. **40**(D1): p. D1178-D1186.
32. Graham, L.A., et al., *Smelt was the likely beneficiary of an antifreeze gene laterally transferred between fishes*. Bmc Evolutionary Biology, 2012. **12**.
33. Grigoriev, I.V., et al., *The Genome Portal of the Department of Energy Joint Genome Institute*. Nucleic Acids Research, 2012. **40**(D1): p. D26-D32.
34. Gulleedge, A.A., et al., *MINING ARABIDOPSIS THALIANA RNA-SEQ DATA WITH INTEGRATED GENOME BROWSER REVEALS STRESS-INDUCED ALTERNATIVE SPLICING OF THE PUTATIVE SPLICING REGULATOR SR45A*. American Journal of Botany, 2012. **99**(2): p. 219-231.
35. Hain, T., et al., *Comparative genomics and transcriptomics of lineages I, II, and III strains of Listeria monocytogenes*. Bmc Genomics, 2012. **13**.
36. Hardison, R.C. and J. Taylor, *Genomic approaches towards finding cis-regulatory modules in animals*. Nature Reviews Genetics, 2012. **13**(7): p. 469-483.
37. Herbig, A., et al., *GenomeRing: alignment visualization based on SuperGenome coordinates*. Bioinformatics, 2012. **28**(12): p. i7-i15.
38. Hertwig, F., et al., *Definition of Genetic Events Directing the Development of Distinct Types of Brain Tumors from Postnatal Neural Stem/Progenitor Cells*. Cancer Research, 2012. **72**(13): p. 3381-3392.
39. Hogart, A., et al., *Genome-wide DNA methylation profiles in hematopoietic stem and progenitor cells reveal overrepresentation of ETS transcription factor binding sites*. Genome Research, 2012. **22**(8): p. 1407-1418.
40. Iguchi-Ishiguro, H., et al., *Analysis of syndecan-1 gene promoter during mouse tooth development*. Archives of Oral Biology, 2012. **57**(5): p. 531-538.
41. Irimia, M., et al., *Extensive conservation of ancient microsynteny across metazoans due to cis-regulatory constraints*. Genome Research, 2012. **22**(12): p. 2356-2367.
42. Ishibashi, M., et al., *Evolutionary growth process of highly conserved sequences in vertebrate genomes*. Gene, 2012. **504**(1): p. 1-5.
43. Islas, J.F., et al., *Transcription factors ETS2 and MESP1 transdifferentiate human dermal fibroblasts into cardiac progenitors*. Proceedings of the National Academy of Sciences of the United States of America, 2012. **109**(32): p. 13016-13021.
44. Itsara, A., et al., *Resolving the Breakpoints of the 17q21.31 Microdeletion Syndrome with Next-Generation Sequencing*. American Journal of Human Genetics, 2012. **90**(4): p. 599-613.
45. Jahangiri, L., A.C. Nelson, and F.C. Wardle, *A cis-regulatory module upstream of deltaC regulated by Ntla and Tbx16 drives expression in the tailbud, presomitic mesoderm and somites*. Developmental Biology, 2012. **371**(1): p. 110-120.
46. Jash, A., et al., *Nuclear Factor of Activated T Cells 1 (NFAT1)-induced Permissive Chromatin Modification Facilitates Nuclear Factor-kappa B (NF-kappa B)-mediated Interleukin-9 (IL-9) Transactivation*. Journal of Biological Chemistry, 2012. **287**(19): p. 15445-15457.
47. Ji, Y., et al., *Catechol O-methyltransferase pharmacogenomics and selective serotonin reuptake inhibitor response*. Pharmacogenomics Journal, 2012. **12**(1): p. 78-85.
48. Jiang, Y., et al., *Analysis of GDSL lipase (GLIP) family genes in rice (*Oryza**

- sativa*). *Plant Omics*, 2012. **5**(4): p. 351-358.
49. Juno, J.A., Y. Keynan, and K.R. Fowke, *Invariant NKT Cells: Regulation and Function during Viral Infection*. *Plos Pathogens*, 2012. **8**(8).
50. Karlsson, M., et al., *Development of Dissolution DNP-MR Substrates for Metabolic Research*. *Applied Magnetic Resonance*, 2012. **43**(1-2): p. 223-236.
51. Keilani, S., et al., *Egr-1 Induces DARPP-32 Expression in Striatal Medium Spiny Neurons via a Conserved Intragenic Element*. *Journal of Neuroscience*, 2012. **32**(20): p. 6808-6818.
52. Khan, A., et al., *The Chloroplast Genome Sequence of Date Palm (*Phoenix dactylifera L. cv. 'Aseel'*)*. *Plant Molecular Biology Reporter*, 2012. **30**(3): p. 666-678.
53. Kiselev, Y., et al., *3T3 Cell Lines Stably Expressing Pax6 or Pax6(5a) - A New Tool Used for Identification of Common and Isoform Specific Target Genes*. *Plos One*, 2012. **7**(2).
54. Kou, S.-J., et al., *Selection and validation of suitable reference genes for miRNA expression normalization by quantitative RT-PCR in citrus somatic embryogenic and adult tissues*. *Plant Cell Reports*, 2012. **31**(12): p. 2151-2163.
55. Lai, Y.Y.Y., et al., *Characterization of the Atlantic salmon (*Salmo salar*) brain-type fatty acid binding protein (fabp7) genes reveals the fates of teleost fabp7 genes following whole genome duplications*. *Gene*, 2012. **504**(2): p. 253-261.
56. Lee, B., et al., *Direct transcriptional regulation of Six6 is controlled by SoxB1 binding to a remote forebrain enhancer*. *Developmental Biology*, 2012. **366**(2): p. 393-403.
57. Lee, C.G., et al., *Interaction of Ets-1 with HDAC1 represses IL-10 expression in Th1 cells (vol 188, pg 2244, 2012)*. *Journal of Immunology*, 2012. **189**(12): p. 5996-5996.
58. Lee, S.-Y., et al., *Characterization of the hamster genomic fragment cloned by TAR cloning technology with interspecific sequence information*. *Genes & Genomics*, 2012. **34**(6): p. 647-652.
59. Liu, Y., N.L. Moskwa, and B. Goffinet, *DEVELOPMENT OF EIGHT MITOCHONDRIAL MARKERS FOR FUNARIACEAE (MUSCI) AND THEIR AMPLIFICATION SUCCESS IN OTHER MOSSES*. *American Journal of Botany*, 2012. **99**(2): p. E62-E65.
60. Lou, P., et al., *Preferential Retention of Circadian Clock Genes during Diploidization following Whole Genome Triplication in *Brassica rapa**. *Plant Cell*, 2012. **24**(6): p. 2415-2426.
61. Luna-Nevarez, P., et al., *Identification of one polymorphism from the PAPP-A2 gene associated to fertility in Romosinuano beef heifers raised under a subtropical environment*. *Revista Mexicana De Ciencias Pecuarias*, 2012. **3**(2): p. 185-200.
62. Maeso, I., et al., *An ancient genomic regulatory block conserved across bilaterians and its dismantling in tetrapods by retrogene replacement*. *Genome Research*, 2012. **22**(4): p. 642-655.
63. Markowitz, V.M., et al., *IMG: the integrated microbial genomes database and comparative analysis system*. *Nucleic Acids Research*, 2012. **40**(D1): p. D115-D122.

64. Matilla, M.A., et al., *Bacterial Biosynthetic Gene Clusters Encoding the Anti-cancer Haterumalide Class of Molecules BIOGENESIS OF THE BROAD SPECTRUM ANTIFUNGAL AND ANTI-OOMYCETE COMPOUND, OOCYDIN A*. Journal of Biological Chemistry, 2012. **287**(46): p. 39125-39138.
65. Meier, S., et al., *Sulfite Action in Glycolytic Inhibition: In Vivo Real-Time Observation by Hyperpolarized <sup>13</sup>C NMR Spectroscopy*. Chembiochem, 2012. **13**(15): p. 2265-2269.
66. Mullen, R.D., S. Park, and S.J. Rhodes, *A Distal Modular Enhancer Complex Acts to Control Pituitary- and Nervous System-Specific Expression of the LHX3 Regulatory Gene*. Molecular Endocrinology, 2012. **26**(2): p. 308-319.
67. Nagel, D.H. and S.A. Kay, *Complexity in the Wiring and Regulation of Plant Circadian Networks*. Current Biology, 2012. **22**(16): p. R648-R657.
68. Nishitsuji, K., et al., *Cell lineage and cis-regulation for a unique GABAergic/glycinergic neuron type in the larval nerve cord of the ascidian Ciona intestinalis*. Development Growth & Differentiation, 2012. **54**(2): p. 177-186.
69. O'Bleness, M.S., et al., *Evolutionary History and Genome Organization of DUF1220 Protein Domains*. G3-Genes Genomes Genetics, 2012. **2**(9): p. 977-986.
70. Ohm, R.A., et al., *Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi*. Plos Pathogens, 2012. **8**(12).
71. Orishchenko, K.E., et al., *A Regulatory Potential of the Xist Gene Promoter in Vole *M. rossiaemeridionalis**. Plos One, 2012. **7**(5).
72. Partridge, S.R., et al., *pEI1573 Carrying bla(IMP-4), from Sydney, Australia, Is Closely Related to Other IncL/M Plasmids*. Antimicrobial Agents and Chemotherapy, 2012. **56**(11): p. 6029-6032.
73. Pharo, E.A., et al., *The mammary gland-specific marsupial ELP and eutherian CTI share a common ancestral gene*. Bmc Evolutionary Biology, 2012. **12**.
74. Philips, S., et al., *Functional Characterization of a Genetic Polymorphism in the Promoter of the ESR2 Gene*. Hormones & Cancer, 2012. **3**(1-2): p. 37-43.
75. Philips, S., et al., *Functional Characterization of a Genetic Polymorphism in the Promoter of the ESR2 Gene*. Hormones & Cancer, 2012. **3**(1-2): p. 37-43.
76. Ragusa, M.A., et al., *In silico characterization of the neural alpha tubulin gene promoter of the sea urchin embryo *Paracentrotus lividus* by phylogenetic footprinting*. Molecular Biology Reports, 2012. **39**(3): p. 2633-2644.
77. Randoux, M., et al., *Gibberellins regulate the transcription of the continuous flowering regulator, RoKSN, a rose TFL1 homologue*. Journal of Experimental Botany, 2012. **63**(18): p. 6543-6554.
78. Reardon, H.T., et al., *Insertion-deletions in a FADS2 intron 1 conserved regulatory locus control expression of fatty acid desaturases 1 and 2 and modulate response to simvastatin*. Prostaglandins Leukotrienes and Essential Fatty Acids, 2012. **87**(1): p. 25-33.
79. Reardon, H.T., et al., *Insertion-deletions in a FADS2 intron 1 conserved regulatory locus control expression of fatty acid desaturases 1 and 2 and modulate response to simvastatin*. Prostaglandins Leukotrienes and Essential Fatty Acids, 2012. **87**(1): p. 25-33.

80. Revanna, K.V., et al., *A web-based multi-genome synteny viewer for customized data*. Bmc Bioinformatics, 2012. **13**.
81. Rhost, S., et al., *Immunomodulatory Type II Natural Killer T Lymphocytes in Health and Disease*. Scandinavian Journal of Immunology, 2012. **76**(3): p. 246-255.
82. Riley, D.R., et al., *Using Sybil for interactive comparative genomics of microbes on the web*. Bioinformatics, 2012. **28**(2): p. 160-166.
83. Rishishwar, L., et al., *Genomic Basis of a Polyagglutinating Isolate of Neisseria meningitidis*. Journal of Bacteriology, 2012. **194**(20): p. 5649-5656.
84. Royo, J.L., et al., *Identification and Analysis of Conserved cis-Regulatory Regions of the MEIS1 Gene*. Plos One, 2012. **7**(3).
85. Sato, S., et al., *Regulation of Six1 expression by evolutionarily conserved enhancers in tetrapods*. Developmental Biology, 2012. **368**(1): p. 95-108.
86. Schanze, D., et al., *Evaluation of conserved and ultra-conserved non-genic sequences in chromosome 15q15-linked periodic catatonia*. American Journal of Medical Genetics Part B-Neuropsychiatric Genetics, 2012. **159B**(1): p. 77-86.
87. Shah, C.A., et al., *HoxA10 Protein Regulates Transcription of Gene Encoding Fibroblast Growth Factor 2 (FGF2) in Myeloid Cells*. Journal of Biological Chemistry, 2012. **287**(22): p. 18230-18248.
88. Smemo, S., et al., *Regulatory variation in a TBX5 enhancer leads to isolated congenital heart disease*. Human Molecular Genetics, 2012. **21**(14): p. 3255-3263.
89. Stolfi, A. and L. Christiaen, *Genetic and Genomic Toolbox of the Chordate Ciona intestinalis*. Genetics, 2012. **192**(1): p. 55-66.
90. Stowe, H.M., et al., *Cloning and expression of porcine Dicer and the impact of developmental stage and culture conditions on MicroRNA expression in porcine embryos*. Gene, 2012. **501**(2): p. 198-205.
91. Timoneda, O., et al., *Determination of Reference microRNAs for Relative Quantification in Porcine Tissues*. Plos One, 2012. **7**(9).
92. Turner, C.A., S.J. Watson, and H. Akil, *The Fibroblast Growth Factor Family: Neuromodulation of Affective Behavior*. Neuron, 2012. **76**(1): p. 160-174.
93. Vasconcelos, E.J.R., et al., *In silico identification of conserved intercoding sequences in Leishmania genomes: Unraveling putative cis-regulatory elements*. Molecular and Biochemical Parasitology, 2012. **183**(2): p. 140-150.
94. Vijayaraj, P., et al., *Erg is a crucial regulator of endocardial-mesenchymal transformation during cardiac valve morphogenesis*. Development, 2012. **139**(21): p. 3973-3985.
95. Wang, J.R., F.P.-M. de Villena, and L. McMillan, *Comparative analysis and visualization of multiple collinear genomes*. Bmc Bioinformatics, 2012. **13**.
96. Wang, W. and L. Christiaen, *TRANSCRIPTIONAL ENHANCERS IN ASCIDIAN DEVELOPMENT*, in *Transcriptional Switches during Development*, S. Plaza and F. Payre, Editors. 2012. p. 147-172.
97. Wang, X., et al., *Human invariant natural killer T cells acquire transient innate responsiveness via histone H4 acetylation induced by weak TCR stimulation*. Journal of Experimental Medicine, 2012. **209**(5): p. 987-1000.
98. Woznica, A., et al., *Initial deployment of the cardiogenic gene regulatory network*

- in the basal chordate, Ciona intestinalis.* Developmental Biology, 2012. **368**(1): p. 127-139.
- 99. Yamashiro, S., et al., *Tropomodulins: Pointed-end capping proteins that regulate actin filament architecture in diverse cell types.* Cytoskeleton, 2012. **69**(6): p. 337-370.
  - 100. Ye, Q., et al., *Isolation of a 97-kb Minimal Essential MHC B Locus from a New Reverse-4D BAC Library of the Golden Pheasant.* Plos One, 2012. **7**(3).
  - 101. Yu, H., et al., *Evolution of coding and non-coding genes in HOX clusters of a marsupial.* Bmc Genomics, 2012. **13**.
  - 102. Zhang, Q., et al., *Genome Sequence of Human Adenovirus Type 55, a Re-Emergent Acute Respiratory Disease Pathogen in China.* Journal of Virology, 2012. **86**(22): p. 12441-12442.
  - 103. Zhang, Q., et al., *Genome Sequence of the First Human Adenovirus Type 14 Isolated in China.* Journal of Virology, 2012. **86**(12): p. 7019-7020.
  - 104. Zhao, L., et al., *Disruption of SoxB1-Dependent Sonic hedgehog Expression in the Hypothalamus Causes Septo-optic Dysplasia.* Developmental Cell, 2012. **22**(3): p. 585-596.
  - 105. Zhuang, X., et al., *Protein genes in repetitive sequence-antifreeze glycoproteins in Atlantic cod genome.* Bmc Genomics, 2012. **13**.
  - 106. Alharbi, R.A., et al., *The role of HOX genes in normal hematopoiesis and acute leukemia.* Leukemia, 2013. **27**(5): p. 1000-1008.
  - 107. Amemiya, C.T. and G.P. Wagner, *Francis (Frank) Hugh Ruddle (1929-2013).* Journal of Experimental Zoology Part B-Molecular and Developmental Evolution, 2013. **320B**(5): p. 273-275.
  - 108. Anwer, M.U. and S.J. Davis, *An overview of natural variation studies in the Arabidopsis thaliana circadian clock.* Seminars in Cell & Developmental Biology, 2013. **24**(5): p. 422-429.
  - 109. Ashman, T.L., A. Kwok, and B.C. Husband, *Revisiting the Dioecy-Polyplody Association: Alternate Pathways and Research Opportunities.* Cytogenetic and Genome Research, 2013. **140**(2-4): p. 241-255.
  - 110. Bekiaris, V., et al., *The Inhibitory Receptor BTLA Controls gamma delta T Cell Homeostasis and Inflammatory Responses.* Immunity, 2013. **39**(6): p. 1082-1094.
  - 111. Bodin, S.S., J.S. Kim, and J.-H. Kim, *Complete Chloroplast Genome of Chionographis japonica (Willd.) Maxim. (Melanthiaceae): Comparative Genomics and Evaluation of Universal Primers for Liliales.* Plant Molecular Biology Reporter, 2013. **31**(6): p. 1407-1421.
  - 112. Bodin, S.S., J.S. Kim, and J.-H. Kim, *Complete Chloroplast Genome of Chionographis japonica (Willd.) Maxim. (Melanthiaceae): Comparative Genomics and Evaluation of Universal Primers for Liliales.* Plant Molecular Biology Reporter, 2013. **31**(6): p. 1407-1421.
  - 113. Boehne, A., et al., *Expression and Sequence Evolution of Aromatase cyp19a1 and Other Sexual Development Genes in East African Cichlid Fishes.* Molecular Biology and Evolution, 2013. **30**(10): p. 2268-2285.
  - 114. Brennan, F.P., et al., *Insights into the low-temperature adaptation and nutritional flexibility of a soil-persistent Escherichia coli.* Fems Microbiology Ecology, 2013. **84**(1): p. 75-85.

115. Brennan, P.J., M. Brigl, and M.B. Brenner, *Invariant natural killer T cells: an innate activation scheme linked to diverse effector functions*. Nature Reviews Immunology, 2013. **13**(2): p. 101-117.
116. Brody, M.J., et al., *Lrrc10 is a novel cardiac-specific target gene of Nkx2-5 and GATA4*. Journal of Molecular and Cellular Cardiology, 2013. **62**: p. 237-246.
117. Bujdoso, N. and S.J. Davis, *Mathematical modeling of an oscillating gene circuit to unravel the circadian clock network of Arabidopsis thaliana*. Frontiers in Plant Science, 2013. **4**.
118. Buzyrapu, R., et al., *BAC-Pool Sequencing and Analysis of Large Segments of A12 and D12 Homoeologous Chromosomes in Upland Cotton*. Plos One, 2013. **8**(10).
119. Campoli, C., et al., *HvLUX1 is a candidate gene underlying the early maturity 10 locus in barley: phylogeny, diversity, and interactions with the circadian clock and photoperiodic pathways*. New Phytologist, 2013. **199**(4): p. 1045-1059.
120. Canestro, C., et al., *Impact of gene gains, losses and duplication modes on the origin and diversification of vertebrates*. Seminars in Cell & Developmental Biology, 2013. **24**(2): p. 83-94.
121. Carre, I. and S.R. Veflingstad, *Emerging design principles in the Arabidopsis circadian clock*. Seminars in Cell & Developmental Biology, 2013. **24**(5): p. 393-398.
122. Chandler, R.L., et al., *ARID1a-DNA Interactions Are Required for Promoter Occupancy by SWI/SNF*. Molecular and Cellular Biology, 2013. **33**(2): p. 265-280.
123. Chantha, S.-C., et al., *Secondary Evolution of a Self-Incompatibility Locus in the Brassicaceae Genus Leavenworthia*. Plos Biology, 2013. **11**(5).
124. Chantha, S.-C., et al., *Secondary Evolution of a Self-Incompatibility Locus in the Brassicaceae Genus Leavenworthia*. Plos Biology, 2013. **11**(5).
125. Chen, H. and X. Wang, *CrusView: A Java-Based Visualization Platform for Comparative Genomics Analyses in Brassicaceae Species*. Plant Physiology, 2013. **163**(1): p. 354-362.
126. Chen, H.Y., et al., *Functional Interaction Between SNPs and Microsatellite in the Transcriptional Regulation of Insulin-Like Growth Factor 1*. Human Mutation, 2013. **34**(9): p. 1289-1297.
127. Chow, B.Y. and S.A. Kay, *Global approaches for telling time: Omics and the Arabidopsis circadian clock*. Seminars in Cell & Developmental Biology, 2013. **24**(5): p. 383-392.
128. Chu, X., et al., *Multiple Microvascular Alterations in Pancreatic Islets and Neuroendocrine Tumors of a Men1 Mouse Model*. American Journal of Pathology, 2013. **182**(6): p. 2355-2367.
129. Conner, J.A., G. Gunawan, and P. Ozias-Akins, *Recombination within the apomixis specific genomic region leads to the uncoupling of apomixis components in Cenchrus ciliaris*. Planta, 2013. **238**(1): p. 51-63.
130. Dalton, R.M., M.H. Koski, and T.-L. Ashman, *Maternal sex effects and inbreeding depression under varied environmental conditions in gynodioecious Fragaria vesca subsp bracteata*. Annals of Botany, 2013. **112**(3): p. 613-621.
131. Das, P.J., et al., *Comparative Organization and Gene Expression Profiles of the Porcine Pseudoautosomal Region*. Cytogenetic and Genome Research, 2013.

- 141(1): p. 26-36.
132. Davis, M.C., *The Deep Homology of the Autopod: Insights from Hox Gene Regulation*. Integrative and Comparative Biology, 2013. **53**(2): p. 224-232.
133. Dawes, L.J., et al., *Wnt-Frizzled Signaling Is Part of an FGF-Induced Cascade that Promotes Lens Fiber Differentiation*. Investigative Ophthalmology & Visual Science, 2013. **54**(3): p. 1582-1590.
134. De Smet, I., et al., *Transcriptional repression of BODENLOS by HD-ZIP transcription factor HB5 in Arabidopsis thaliana*. Journal of Experimental Botany, 2013. **64**(10): p. 3009-3019.
135. De Smet, I., et al., *Transcriptional repression of BODENLOS by HD-ZIP transcription factor HB5 in Arabidopsis thaliana*. Journal of Experimental Botany, 2013. **64**(10): p. 3009-3019.
136. Debiais-Thibaud, M., et al., *Heterogeneous Conservation of Dlx Paralog Co-Expression in Jawed Vertebrates*. Plos One, 2013. **8**(6).
137. Dehghan, S., et al., *Simian adenovirus type 35 has a recombinant genome comprising human and simian adenovirus sequences, which predicts its potential emergence as a human respiratory pathogen*. Virology, 2013. **447**(1-2): p. 265-273.
138. Deng, Z.-B., et al., *Exosome-like Nanoparticles from Intestinal Mucosal Cells Carry Prostaglandin E-2 and Suppress Activation of Liver NKT Cells*. Journal of Immunology, 2013. **190**(7): p. 3579-3589.
139. Dickel, D.E., A. Visel, and L.A. Pennacchio, *Functional anatomy of distant-acting mammalian enhancers*. Philosophical Transactions of the Royal Society B-Biological Sciences, 2013. **368**(1620).
140. Diepeveen, E.T., O. Roth, and W. Salzburger, *Immune-Related Functions of the Hivep Gene Family in East African Cichlid Fishes*. G3-Genes Genomes Genetics, 2013. **3**(12): p. 2205-2217.
141. Diepeveen, E.T., O. Roth, and W. Salzburger, *Immune-Related Functions of the Hivep Gene Family in East African Cichlid Fishes*. G3-Genes Genomes Genetics, 2013. **3**(12): p. 2205-2217.
142. Ding, X., et al., *Signaling between Transforming Growth Factor beta (TGF-beta) and Transcription Factor SNAI2 Represses Expression of MicroRNA miR-203 to Promote Epithelial-Mesenchymal Transition and Tumor Metastasis*. Journal of Biological Chemistry, 2013. **288**(15): p. 10241-10253.
143. Doglio, L., et al., *Parallel Evolution of Chordate Cis-Regulatory Code for Development*. Plos Genetics, 2013. **9**(11).
144. Dong, W., et al., *Complete Chloroplast Genome of Sedum sarmentosum and Chloroplast Genome Evolution in Saxifragales*. Plos One, 2013. **8**(10).
145. Donner, T.J. and E. Scarpella, *Transcriptional control of early vein expression of CYCA2; 1 and CYCA2;4 in Arabidopsis leaves*. Mechanisms of Development, 2013. **130**(1): p. 14-24.
146. Droegemöller, B.I., et al., *Next-generation sequencing of pharmacogenes: a critical analysis focusing on schizophrenia treatment*. Pharmacogenetics and Genomics, 2013. **23**(12): p. 666-674.
147. Dubchak, I., et al., *Whole-Genome rVISTA: a tool to determine enrichment of transcription factor binding sites in gene promoters from transcriptomic data*.

- Bioinformatics, 2013. **29**(16): p. 2059-2061.
148. Dudazy-Gralla, S., et al., *Identification of thyroid hormone response elements in vivo using mice expressing a tagged thyroid hormone receptor alpha 1*. Bioscience Reports, 2013. **33**: p. 295-302.
149. Dwyer, K.G., et al., *Molecular Characterization and Evolution of Self-Incompatibility Genes in Arabidopsis thaliana: The Case of the Sc Haplotype*. Genetics, 2013. **193**(3): p. 985-U526.
150. Ekanayake, P.N., et al., *Phylogenomics of fescue grass-derived fungal endophytes based on selected nuclear genes and the mitochondrial gene complement*. Bmc Evolutionary Biology, 2013. **13**.
151. Fahlgren, N., et al., *Phytophthora Have Distinct Endogenous Small RNA Populations That Include Short Interfering and microRNAs*. Plos One, 2013. **8**(10).
152. Falvo, J.V., et al., *Epigenetic Control of Cytokine Gene Expression: Regulation of the TNF/LT Locus and T Helper Cell Differentiation*, in *Advances in Immunology*, Vol 118, F.W. Alt, Editor. 2013. p. 37-128.
153. Fang, G.-C., et al., *A physical map of the Chinese chestnut (Castanea mollissima) genome and its integration with the genetic map*. Tree Genetics & Genomes, 2013. **9**(2): p. 525-537.
154. Farre, E.M. and T. Liu, *The PRR family of transcriptional regulators reflects the complexity and evolution of plant circadian clocks*. Current Opinion in Plant Biology, 2013. **16**(5): p. 621-629.
155. Fatima, A. and D.G. Morris, *MicroRNAs in domestic livestock*. Physiological Genomics, 2013. **45**(16): p. 685-696.
156. Fior, S., et al., *Spatiotemporal reconstruction of the Aquilegia rapid radiation through next-generation sequencing of rapidly evolving cpDNA regions*. New Phytologist, 2013. **198**(2): p. 579-592.
157. Friese, R.S., et al., *MicroRNA-22 and promoter motif polymorphisms at the Chga locus in genetic hypertension: functional and therapeutic implications for gene expression and the pathogenesis of hypertension*. Human Molecular Genetics, 2013. **22**(18): p. 3624-3640.
158. Galagan, J., A. Lyubetskaya, and A. Gomes, *ChIP-Seq and the Complexity of Bacterial Transcriptional Regulation*, in *Systems Biology*, M.G. Katze, Editor. 2013. p. 43-68.
159. Gapin, L., D.I. Godfrey, and J. Rossjohn, *Natural Killer T cell obsession with self-antigens*. Current Opinion in Immunology, 2013. **25**(2): p. 168-173.
160. Garrett-Sinha, L.A., *Review of Ets1 structure, function, and roles in immunity*. Cellular and Molecular Life Sciences, 2013. **70**(18): p. 3375-3390.
161. Gery, S. and H.P. Koeffler, *Role of the adaptor protein LNK in normal and malignant hematopoiesis*. Oncogene, 2013. **32**(26): p. 3111-3118.
162. Gonthier, L., et al., *High-density genetic maps for loci involved in nuclear male sterility (NMS1) and sporophytic self-incompatibility (S-locus) in chicory (Cichorium intybus L., Asteraceae)*. Theoretical and Applied Genetics, 2013. **126**(8): p. 2103-2121.
163. Goossens, V.J., *Adenovirus-36 prevalence paradox in development*. Journal of Clinical Virology, 2013. **56**(1): p. 5-6.

164. Haas, B.J., et al., *De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis*. Nature Protocols, 2013. **8**(8): p. 1494-1512.
165. Hamilton, N.A., I. Tammen, and H.W. Raadsma, *Multi-Species Comparative Analysis of the Equine ACE Gene Identifies a Highly Conserved Potential Transcription Factor Binding Site in Intron 16*. Plos One, 2013. **8**(2).
166. Hand, M.L., et al., *Plastome Sequence Determination and Comparative Analysis for Members of the Lolium-Festuca Grass Species Complex*. G3-Genes Genomes Genetics, 2013. **3**(4): p. 607-616.
167. Hand, M.L., et al., *Plastome Sequence Determination and Comparative Analysis for Members of the Lolium-Festuca Grass Species Complex*. G3-Genes Genomes Genetics, 2013. **3**(4): p. 607-616.
168. Harmston, N., A. Baresic, and B. Lenhard, *The mystery of extreme non-coding conservation*. Philosophical Transactions of the Royal Society B-Biological Sciences, 2013. **368**(1632).
169. Hashimoto, K., et al., *Human Stearoyl-CoA Desaturase 1 (SCD-1) Gene Expression Is Negatively Regulated by Thyroid Hormone without Direct Binding of Thyroid Hormone Receptor to the Gene Promoter*. Endocrinology, 2013. **154**(1): p. 537-549.
170. Haydon, M.J., et al., *Metabolic regulation of circadian clocks*. Seminars in Cell & Developmental Biology, 2013. **24**(5): p. 414-421.
171. Hervey, W.M., J.T. Stewart, and G. Catalano, *Diagnosis and management of periodic catatonia*. Journal of Psychiatry & Neuroscience, 2013. **38**(3): p. E7-E8.
172. Hosseini, P., I. Ovcharenko, and B.F. Matthews, *Using an ensemble of statistical metrics to quantify large sets of plant transcription factor binding sites*. Plant Methods, 2013. **9**.
173. Hotta, C.T., M.Y. Nishiyama, Jr., and G.M. Souza, *Circadian Rhythms of Sense and Antisense Transcription in Sugarcane, a Highly Polyploid Crop*. Plos One, 2013. **8**(8).
174. Hu, L., et al., *Increased Fanconi C expression contributes to the emergency granulopoiesis response*. Journal of Clinical Investigation, 2013. **123**(9): p. 3952-3966.
175. Huang, Y.-Y., A.J.M. Matzke, and M. Matzke, *Complete Sequence and Comparative Analysis of the Chloroplast Genome of Coconut Palm (Cocos nucifera)*. Plos One, 2013. **8**(8).
176. Hummer, K.E., et al., *Asian Germplasm Influences on American Berry Crops*. Hortscience, 2013. **48**(9): p. 1090-1094.
177. Hupalo, D. and A.D. Kern, *Conservation and Functional Element Discovery in 20 Angiosperm Plant Genomes*. Molecular Biology and Evolution, 2013. **30**(7): p. 1729-1744.
178. Iglesias-Fernandez, R., et al., *Arabidopsis thaliana bZIP44: a transcription factor affecting seed germination and expression of the mannanase-encoding gene AtMAN7*. Plant Journal, 2013. **74**(5): p. 767-780.
179. Ikeda, D., et al., *Lampreys Have a Single Gene Cluster for the Fast Skeletal Myosin Heavy Chain Gene Family*. Plos One, 2013. **8**(12).
180. Imamura, M., et al., *Myocardin and microRNA-1 modulate bladder activity*

- through connexin 43 expression during post-natal development.* Journal of Cellular Physiology, 2013. **228**(9): p. 1819-1826.
- 181. Irimia, M., et al., *Ancient cis-regulatory constraints and the evolution of genome architecture.* Trends in Genetics, 2013. **29**(9): p. 521-528.
  - 182. Ishikawa, G., et al., *Molecular characterization of spontaneous and induced mutations in the three homoeologous waxy genes of Japanese barnyard millet Echinochloa esculenta (A. Braun) H. Scholz.* Molecular Breeding, 2013. **31**(1): p. 69-78.
  - 183. Jose-Edwards, D.S., et al., *Tbx2/3 is an essential mediator within the Brachyury gene network during Ciona notochord development.* Development, 2013. **140**(11): p. 2422-2433.
  - 184. Kanda, M., T. Ikeda, and S. Fujiwara, *Identification of a retinoic acid-responsive neural enhancer in the Ciona intestinalis Hox1 gene.* Development Growth & Differentiation, 2013. **55**(2): p. 260-269.
  - 185. Kawakami, Y., et al., *A small interfering RNA targeting Lnk accelerates bone fracture healing with early neovascularization.* Laboratory Investigation, 2013. **93**(9): p. 1036-1053.
  - 186. Khan, M.R. and G.M. Ali, *Functional evolution of cis-regulatory modules of STMADS11 superclade MADS-box genes.* Plant Molecular Biology, 2013. **83**(4-5): p. 489-506.
  - 187. Kim, Y., et al., *ELF4 Regulates GIGANTEA Chromatin Access through Subnuclear Sequestration.* Cell Reports, 2013. **3**(3): p. 671-677.
  - 188. Kitchen, C.M., et al., *Expression and promoter analysis of a highly restricted integrin alpha gene in vascular smooth muscle.* Gene, 2013. **513**(1): p. 82-89.
  - 189. Koptyug, I.V., *Spin hyperpolarization in NMR to address enzymatic processes in vivo.* Mendeleev Communications, 2013. **23**(6): p. 299-312.
  - 190. Ku, C., et al., *The Complete Plastid Genome Sequence of Madagascar Periwinkle Catharanthus roseus (L.) G. Don: Plastid Genome Evolution, Molecular Marker Identification, and Phylogenetic Implications in Asterids.* Plos One, 2013. **8**(6).
  - 191. Ku, C., J.-M. Hu, and C.-H. Kuo, *Complete Plastid Genome Sequence of the Basal Asterid Ardisia polysticta Miq. and Comparative Analyses of Asterid Plastid Genomes.* Plos One, 2013. **8**(4).
  - 192. Kumar, S., et al., *Differential Expression of Rice Lambda Class GST Gene Family Members During Plant Growth, Development, and in Response to Stress Conditions.* Plant Molecular Biology Reporter, 2013. **31**(3): p. 569-580.
  - 193. Laimer, J., et al., *D-Light on promoters: a client-server system for the analysis and visualization of cis-regulatory elements.* Bmc Bioinformatics, 2013. **14**.
  - 194. Lawley, B., I.M. Sims, and G.W. Tannock, *Whole-Transcriptome Shotgun Sequencing (RNA-seq) Screen Reveals Upregulation of Cellobiose and Motility Operons of Lactobacillus ruminis L5 during Growth on Tetrasaccharides Derived from Barley beta-Glucan.* Applied and Environmental Microbiology, 2013. **79**(18): p. 5661-5669.
  - 195. Lechat, P., E. Souche, and I. Moszer, *SynTView - an interactive multi-view genome browser for next-generation comparative microorganism genomics.* Bmc Bioinformatics, 2013. **14**.

196. Lechat, P., E. Souche, and I. Moszer, *SynTView - an interactive multi-view genome browser for next-generation comparative microorganism genomics*. Bmc Bioinformatics, 2013. **14**.
197. Lee, T.-H., et al., *PGDD: a database of gene and genome duplication in plants*. Nucleic Acids Research, 2013. **41**(D1): p. D1152-D1158.
198. Li, M.-W., et al., *Silicon Era of Carbon-Based Life: Application of Genomics and Bioinformatics in Crop Stress Research*. International Journal of Molecular Sciences, 2013. **14**(6): p. 11444-11483.
199. Li, Q., et al., *An Intragenic SRF-Dependent Regulatory Motif Directs Cardiac-Specific microRNA-1-1/133a-2 Expression*. Plos One, 2013. **8**(9).
200. Li, R., et al., *Complete Sequencing of Five Araliaceae Chloroplast Genomes and the Phylogenetic Implications*. Plos One, 2013. **8**(10).
201. Li, W., et al., *LEAFY Controls Auxin Response Pathways in Floral Primordium Formation*. Science Signaling, 2013. **6**(277).
202. Li, W., et al., *LEAFY Controls Auxin Response Pathways in Floral Primordium Formation*. Science Signaling, 2013. **6**(270).
203. Li, Y., et al., *Plasticity of Leukocytic Exudates in Resolving Acute Inflammation Is Regulated by MicroRNA and Proresolving Mediators*. Immunity, 2013. **39**(5): p. 885-898.
204. Lin, G., et al., *NF-kappa B Is Activated in CD4(+) iNKT Cells by Sickle Cell Disease and Mediates Rapid Induction of Adenosine A(2A) Receptors*. Plos One, 2013. **8**(10).
205. Liu, Y., et al., *Complete Chloroplast Genome Sequences of Mongolia Medicine Artemisia frigida and Phylogenetic Relationships with Other Plants*. Plos One, 2013. **8**(2).
206. Long, X., S.L. Cowan, and J.M. Miano, *Mitogen-Activated Protein Kinase 14 Is a Novel Negative Regulatory Switch for the Vascular Smooth Muscle Cell Contractile Gene Program*. Arteriosclerosis Thrombosis and Vascular Biology, 2013. **33**(2): p. 378-+.
207. Loots, G.G., et al., *Interrogating Transcriptional Regulatory Sequences in Tol2-Mediated Xenopus Transgenics*. Plos One, 2013. **8**(7).
208. Lukas, B. and J. Novak, *The complete chloroplast genome of Origanum vulgare L. (Lamiaceae)*. Gene, 2013. **528**(2): p. 163-169.
209. Maeso, I., et al., *Deep conservation of cis-regulatory elements in metazoans*. Philosophical Transactions of the Royal Society B-Biological Sciences, 2013. **368**(1632).
210. Maricic, T., et al., *A Recent Evolutionary Change Affects a Regulatory Element in the Human FOXP2 Gene*. Molecular Biology and Evolution, 2013. **30**(4): p. 844-852.
211. Martin, G., et al., *The Complete Chloroplast Genome of Banana (*Musa acuminata*, Zingiberales): Insight into Plastid Monocotyledon Evolution*. Plos One, 2013. **8**(6).
212. Mazur, M.A., et al., *Microphthalmia Transcription Factor Regulates Pancreatic beta-Cell Function*. Diabetes, 2013. **62**(8): p. 2834-2842.
213. Mehta, T.K., et al., *Evidence for at least six Hox clusters in the Japanese lamprey (*Lethenteron japonicum*)*. Proceedings of the National Academy of Sciences of

- the United States of America, 2013. **110**(40): p. 16044-16049.
214. Mehta, T.K., et al., *Evidence for at least six Hox clusters in the Japanese lamprey (*Lethenteron japonicum*)*. Proceedings of the National Academy of Sciences of the United States of America, 2013. **110**(40): p. 16044-16049.
215. Mendes, M.A., et al., *MADS Domain Transcription Factors Mediate Short-Range DNA Looping That Is Essential for Target Gene Expression in Arabidopsis*. Plant Cell, 2013. **25**(7): p. 2560-2572.
216. Mlera, L., et al., *Whole-genome consensus sequence analysis of a South African rotavirus SA11 sample reveals a mixed infection with two close derivatives of the SA11-H96 strain*. Archives of Virology, 2013. **158**(5): p. 1021-1030.
217. Moore, S., et al., *Distinct Regulatory Mechanisms Act to Establish and Maintain Pax3 Expression in the Developing Neural Tube*. Plos Genetics, 2013. **9**(10).
218. Nakano, M., et al., *Characterization of genes associated with polyembryony and in vitro somatic embryogenesis in Citrus*. Tree Genetics & Genomes, 2013. **9**(3): p. 795-803.
219. Napolitano, A., et al., *Functional Education of Invariant NKT Cells by Dendritic Cell Tuning of SHP-1*. Journal of Immunology, 2013. **190**(7): p. 3299-3308.
220. Navarrete, K., et al., *TCF4 (e2-2; ITF2): A schizophrenia-associated gene with pleiotropic effects on human disease*. American Journal of Medical Genetics Part B-Neuropsychiatric Genetics, 2013. **162B**(1): p. 1-16.
221. Niebler, S. and A.K. Bosserhoff, *The transcription factor activating enhancer-binding protein epsilon (AP-2 epsilon) regulates the core promoter of type II collagen (COL2A1)*. Febs Journal, 2013. **280**(6): p. 1397-1408.
222. Oberlin, A.T., et al., *Biological Database of Images and Genomes: tools for community annotations linking image and genomic information*. Database-the Journal of Biological Databases and Curation, 2013.
223. Oh-Hashi, K., et al., *Characterization of the 5'-flanking region of the mouse asparagine-linked glycosylation 12 homolog gene*. Cellular & Molecular Biology Letters, 2013. **18**(3): p. 315-327.
224. Pascual-Anaya, J., et al., *Evolution of Hox gene clusters in deuterostomes*. Bmc Developmental Biology, 2013. **13**.
225. Patnala, R., J. Clements, and J. Batra, *Candidate gene association studies: a comprehensive guide to useful in silico tools*. Bmc Genetics, 2013. **14**.
226. Perez-Santangelo, S., R.G. Schlaen, and M.J. Yanovsky, *Genomic analysis reveals novel connections between alternative splicing and circadian regulatory networks*. Briefings in Functional Genomics, 2013. **12**(1): p. 13-24.
227. Powell, D.R., et al., *Prdm1a directly activates foxd3 and tfap2a during zebrafish neural crest specification*. Development, 2013. **140**(16): p. 3445-3455.
228. Prychid, C.J. and J.J. Bruhl, *Floral ontogeny and gene protein localization rules out euanthial interpretation of reproductive units in Lepironia (Cyperaceae, Mapanioideae, Chrysitrichae)*. Annals of Botany, 2013. **112**(1): p. 161-177.
229. Qian, J., et al., *The Complete Chloroplast Genome Sequence of the Medicinal Plant Salvia miltiorrhiza*. Plos One, 2013. **8**(2).
230. Qian, J., et al., *The Complete Chloroplast Genome Sequence of the Medicinal Plant Salvia miltiorrhiza*. Plos One, 2013. **8**(2).
231. Qin, L.J., Y. Lv, and Q.Y. Huang, *Meta-analysis of association of common*

- variants in the KCNJ11-ABCC8 region with type 2 diabetes.* Genetics and Molecular Research, 2013. **12**(3): p. 2990-3002.
232. Randall, T.A., et al., *Genomic, RNAseq, and Molecular Modeling Evidence Suggests That the Major Allergen Domain in Insects Evolved from a Homodimeric Origin.* Genome Biology and Evolution, 2013. **5**(12): p. 2344-2358.
233. Ravi, V., et al., *Sequencing of Pax6 Loci from the Elephant Shark Reveals a Family of Pax6 Genes in Vertebrate Genomes, Forged by Ancient Duplications and Divergences.* Plos Genetics, 2013. **9**(1).
234. Renzette, N., et al., *Rapid Intrahost Evolution of Human Cytomegalovirus Is Shaped by Demography and Positive Selection.* Plos Genetics, 2013. **9**(9).
235. Risseeuw, E., et al., *An Activated Form of UFO Alters Leaf Development and Produces Ectopic Floral and Inflorescence Meristems.* Plos One, 2013. **8**(12).
236. Rizzi, T.S., et al., *FADS2 Genetic Variance in Combination with Fatty Acid Intake Might Alter Composition of the Fatty Acids in Brain.* Plos One, 2013. **8**(6).
237. Robinson, C.M., et al., *Molecular evolution of human adenoviruses.* Scientific Reports, 2013. **3**.
238. Robinson, C.M., et al., *Predicting the Next Eye Pathogen: Analysis of a Novel Adenovirus.* Mbio, 2013. **4**(2).
239. Rosin, J.M., S. Abassah-Oppong, and J. Cobb, *Comparative transgenic analysis of enhancers from the human SHOX and mouse Shox2 genomic regions.* Human Molecular Genetics, 2013. **22**(15): p. 3063-3076.
240. Roux, C., et al., *Recent and Ancient Signature of Balancing Selection around the S-Locus in Arabidopsis halleri and A. lyrata.* Molecular Biology and Evolution, 2013. **30**(2): p. 435-447.
241. Roux, C., et al., *Crossing the Species Barrier: Genomic Hotspots of Introgression between Two Highly Divergent Ciona intestinalis Species.* Molecular Biology and Evolution, 2013. **30**(7): p. 1574-1587.
242. Ruffner, B., et al., *Oral insecticidal activity of plant-associated pseudomonads.* Environmental Microbiology, 2013. **15**(3): p. 751-763.
243. Rughone, M.L., et al., *LNK genes integrate light and clock signaling networks at the core of the Arabidopsis oscillator.* Proceedings of the National Academy of Sciences of the United States of America, 2013. **110**(29): p. 12120-12125.
244. Saerkinen, T. and M. George, *Plastid Marker Variation: Can Complete Plastid Genomes from Closely Related Species Help?* Plos One, 2013. **8**(11).
245. Sakurai, D., et al., *Preferential Binding to Elk-1 by SLE-Associated IL10 Risk Allele Upregulates IL10 Expression.* Plos Genetics, 2013. **9**(10).
246. Salamone, I., et al., *BIOCLIMATIC, ECOLOGICAL, AND PHENOTYPIC INTERMEDIACY AND HIGH GENETIC ADMIXTURE IN A NATURAL HYBRID OF OCTOPLOID STRAWBERRIES.* American Journal of Botany, 2013. **100**(5): p. 939-950.
247. Salem, T., et al., *Chromatin loop organization of the junb locus in mouse dendritic cells.* Nucleic Acids Research, 2013. **41**(19): p. 8908-8925.
248. Sanchez-Villagra, M.R., *Why are There Fewer Marsupials than Placental? On the Relevance of Geography and Physiology to Evolutionary Patterns of Mammalian Diversity and Disparity.* Journal of Mammalian Evolution, 2013. **20**(4): p. 279-290.

249. Sanges, R., et al., *Highly conserved elements discovered in vertebrates are present in non-syntenic loci of tunicates, act as enhancers and can be transcribed during development*. Nucleic Acids Research, 2013. **41**(6): p. 3600-3618.
250. Sassi, M. and T. Vernoux, *Auxin and self-organization at the shoot apical meristem*. Journal of Experimental Botany, 2013. **64**(9): p. 2579-2592.
251. Schneider, I. and N.H. Shubin, *The origin of the tetrapod limb: from expeditions to enhancers*. Trends in Genetics, 2013. **29**(7): p. 419-426.
252. Scott, J.C., et al., *A Two-Component System Regulates Hemin Acquisition in Porphyromonas gingivalis*. Plos One, 2013. **8**(9).
253. Shah, C.A., et al., *The Leukemia-associated Mll-Ell Oncoprotein Induces Fibroblast Growth Factor 2 (Fgf2)-dependent Cytokine Hypersensitivity in Myeloid Progenitor Cells*. Journal of Biological Chemistry, 2013. **288**(45): p. 32490-32505.
254. Shaham, O., et al., *Pax6 Regulates Gene Expression in the Vertebrate Lens through miR-204*. Plos Genetics, 2013. **9**(3).
255. Sharma, N., P.L. Bhalla, and M.B. Singh, *Transcriptome-wide profiling and expression analysis of transcription factor families in a liverwort, Marchantia polymorpha*. Bmc Genomics, 2013. **14**.
256. Shin, J., M.U. Anwer, and S.J. Davis, *Phytochrome-Interacting Factors (PIFs) as Bridges between Environmental Signals and the Circadian Clock: Diurnal Regulation of Growth and Development*. Molecular Plant, 2013. **6**(3): p. 592-595.
257. Shin, J., et al., *Overexpression and Loss-of-function at TIME FOR COFFEE Results in Similar Phenotypes in Diverse Growth and Physiological Responses*. Journal of Plant Biology, 2013. **56**(3): p. 152-159.
258. Simoes-Costa, M. and M.E. Bronner, *Insights into neural crest development and evolution from genomic analysis*. Genome Research, 2013. **23**(7): p. 1069-1080.
259. Singh, G., et al., *Homologous Recombination in E3 Genes of Human Adenovirus Species D*. Journal of Virology, 2013. **87**(22): p. 12481-12488.
260. Soeker, T. and A. Goedecke, *Expression of the murine Nr4a1 gene is controlled by three distinct genomic loci*. Gene, 2013. **512**(2): p. 517-520.
261. Soltis, D.E., et al., *The potential of genomics in plant systematics*. Taxon, 2013. **62**(5): p. 886-898.
262. Sone, M., et al., *A modified UPR stress sensing system reveals a novel tissue distribution of IRE1/XBP1 activity during normal Drosophila development*. Cell Stress & Chaperones, 2013. **18**(3): p. 307-319.
263. Spangenberg, L., et al., *Polysome profiling shows extensive posttranscriptional regulation during human adipocyte stem cell differentiation into adipocytes*. Stem Cell Research, 2013. **11**(2): p. 902-912.
264. Stull, G.W., et al., *A TARGETED ENRICHMENT STRATEGY FOR MASSIVELY PARALLEL SEQUENCING OF ANGIOSPERM PLASTID GENOMES*. Applications in Plant Sciences, 2013. **1**(2).
265. Sun, Y.-x., et al., *Complete Plastid Genome Sequencing of Trochodendraceae Reveals a Significant Expansion of the Inverted Repeat and Suggests a Paleogene Divergence between the Two Extant Species*. Plos One, 2013. **8**(4).
266. Symonova, R., et al., *Molecular Cytogenetics in Artificial Hybrid and Highly*

- Polyplid Sturgeons: An Evolutionary Story Narrated by Repetitive Sequences.* Cytogenetic and Genome Research, 2013. **141**(2-3): p. 153-162.
267. Tang, L., et al., *Genome and Bioinformatic Analysis of a HAdV-B14p1 Virus Isolated from a Baby with Pneumonia in Beijing, China.* Plos One, 2013. **8**(3).
268. Tani, S., et al., *Developmental expression and evolution of muscle-specific microRNAs conserved in vertebrates.* Evolution & Development, 2013. **15**(4): p. 293-304.
269. Taveirne, M.E., et al., *The Complete Campylobacter jejuni Transcriptome during Colonization of a Natural Host Determined by RNAseq.* Plos One, 2013. **8**(8).
270. Tennessen, J.A., et al., *Targeted Sequence Capture Provides Insight into Genome Structure and Genetics of Male Sterility in a Gynodioecious Diploid Strawberry, Fragaria vesca ssp bracteata (Rosaceae).* G3-Genes Genomes Genetics, 2013. **3**(8): p. 1341-1351.
271. Thein, S.L., *Genetic association studies in beta-hemoglobinopathies.* Hematology-American Society of Hematology Education Program, 2013: p. 354-361.
272. Tripurani, S.K., et al., *BMP-specific SMADs function as novel repressors of PDGFA and modulate its expression in ovarian granulosa cells and tumors.* Oncogene, 2013. **32**(33): p. 3877-3885.
273. Ungvari, Z., et al., *Aging-Induced Dysregulation of Dicer1-Dependent MicroRNA Expression Impairs Angiogenic Capacity of Rat Cerebromicrovascular Endothelial Cells.* Journals of Gerontology Series a-Biological Sciences and Medical Sciences, 2013. **68**(8): p. 877-891.
274. Vadasz, S., et al., *Pax7 is regulated by cMyb during early neural crest development through a novel enhancer.* Development, 2013. **140**(17): p. 3691-3702.
275. Vahl, J.C., et al., *NKT Cell-TCR Expression Activates Conventional T Cells in Vivo, but Is Largely Dispensable for Mature NKT Cell Biology.* Plos Biology, 2013. **11**(6).
276. Vasquez-Dunddel, D., et al., *STAT3 regulates arginase-I in myeloid-derived suppressor cells from cancer patients.* Journal of Clinical Investigation, 2013. **123**(4): p. 1580-1589.
277. Villeneuve, C., et al., *Methylophaga nitratireducenscens sp. nov. and Methylophaga frappieri sp. nov., isolated from the biofilm of the methanol-fed denitrification system treating the seawater at the Montreal Biodome.* International Journal of Systematic and Evolutionary Microbiology, 2013. **63**: p. 2216-2222.
278. Villota-Herdoiza, D., et al., *Transcriptional regulation of teleost Aicda genes. Part 1-Suppressors of promiscuous promoters.* Fish & Shellfish Immunology, 2013. **35**(6): p. 1981-1987.
279. von Kohn, C., A. Kielkowska, and M.J. Havey, *Sequencing and annotation of the chloroplast DNAs and identification of polymorphisms distinguishing normal male-fertile and male-sterile cytoplasms of onion.* Genome, 2013. **56**(12): p. 737-742.
280. Wang, J., et al., *A brief introduction to web-based genome browsers.* Briefings in Bioinformatics, 2013. **14**(2): p. 131-143.

281. Wang, S., C. Shi, and L.-Z. Gao, *Plastid Genome Sequence of a Wild Woody Oil Species, Prinsepia utilis, Provides Insights into Evolutionary and Mutational Patterns of Rosaceae Chloroplast Genomes*. Plos One, 2013. **8**(9).
282. Wang, T., et al., *STAR: an integrated solution to management and visualization of sequencing data*. Bioinformatics, 2013. **29**(24): p. 3204-3210.
283. Wang, W., et al., *NK4 Antagonizes Tbx1/10 to Promote Cardiac versus Pharyngeal Muscle Fate in the Ascidian Second Heart Field*. Plos Biology, 2013. **11**(12).
284. Wei, L., et al., *Nannochloropsis plastid and mitochondrial phylogenomes reveal organelle diversification mechanism and intragenus phylotyping strategy in microalgae*. Bmc Genomics, 2013. **14**.
285. Wen, J., et al., *Biogeography: Where do we go from here?* Taxon, 2013. **62**(5): p. 912-927.
286. Whittle, C.A. and H. Johannesson, *Evolutionary Dynamics of Sex-Biased Genes in a Hermaphrodite Fungus*. Molecular Biology and Evolution, 2013. **30**(11): p. 2435-2446.
287. Wuyun, T., et al., *A phylogenetic network of wild Ussurian pears (*Pyrus ussuriensis Maxim.*) in China revealed by hypervariable regions of chloroplast DNA*. Tree Genetics & Genomes, 2013. **9**(1): p. 167-177.
288. Yamaguchi, N. and Y. Komeda, *The role of CORYMBOSA1/BIG and auxin in the growth of *Arabidopsis* pedicel and internode*. Plant Science, 2013. **209**: p. 64-74.
289. Yang, J.-B., et al., *Comparative Chloroplast Genomes of Camellia Species*. Plos One, 2013. **8**(8).
290. Yi, X., et al., *The Complete Chloroplast Genome Sequence of *Cephalotaxus oliveri* (Cephalotaxaceae): Evolutionary Comparison of *Cephalotaxus* Chloroplast DNAs and Insights into the Loss of Inverted Repeat Copies in Gymnosperms*. Genome Biology and Evolution, 2013. **5**(4): p. 688-698.
291. Zhang, H., et al., *Insights from the Complete Chloroplast Genome into the Evolution of *Sesamum indicum* L.* Plos One, 2013. **8**(11).
292. Zhang, X., et al., *SAHA, an HDAC Inhibitor, Attenuates Antibody-Mediated Allograft Rejection*. Transplantation, 2013. **96**(6): p. 529-537.
293. Zhang, X., et al., *Identification of a Genetic Determinant in Clinical *Enterococcus faecium* Strains That Contributes to Intestinal Colonization During Antibiotic Treatment*. Journal of Infectious Diseases, 2013. **207**(11): p. 1780-1786.
294. Zhao, X.Q., et al., *Complete mitochondrial genome of the aluminum-tolerant fungus *Rhodotorula taiwanensis* RS1 and comparative analysis of Basidiomycota mitochondrial genomes*. Microbiologyopen, 2013. **2**(2): p. 308-317.
295. Zhu, Z., et al., *MGAViewer: a desktop visualization tool for analysis of metagenomics alignment data*. Bioinformatics, 2013. **29**(1): p. 122-123.
296. Zou, F., et al., *Linking Protective GAB2 Variants, Increased Cortical GAB2 Expression and Decreased Alzheimer's Disease Pathology*. Plos One, 2013. **8**(5).
297. Abbas, A.K., et al., *Negative regulation of the peptidylarginine deiminase type IV promoter by NF-kappa B in human myeloid cells*. Gene, 2014. **533**(1): p. 123-131.
298. Aderhold, A., D. Husmeier, and M. Grzegorczyk, *Statistical inference of regulatory networks for circadian regulation*. Statistical Applications in Genetics

- and Molecular Biology, 2014. **13**(3): p. 227-273.
299. Allcock, R.J.N., *Production and Analytic Bioinformatics for Next-Generation DNA Sequencing*, in *Clinical Bioinformatics, 2nd Edition*, R. Trent, Editor. 2014. p. 17-29.
300. Anwer, M.U., et al., *Natural variation reveals that intracellular distribution of ELF3 protein is associated with function in the circadian clock*. Elife, 2014. **3**.
301. Aryal, B., N. Rotllan, and C. Fernandez-Hernando, *Noncoding RNAs and Atherosclerosis*. Current Atherosclerosis Reports, 2014. **16**(5).
302. Ashfield, T., et al., *Evolutionary Relationship of Disease Resistance Genes in Soybean and Arabidopsis Specific for the Pseudomonas syringae Effectors AvrB and AvrRpm1*. Plant Physiology, 2014. **166**(1): p. 235-251.
303. Azim, M.K., I.A. Khan, and Y. Zhang, *Characterization of mango (*Mangifera indica L.*) transcriptome and chloroplast genome*. Plant Molecular Biology, 2014. **85**(1-2): p. 193-208.
304. Balasubramani, A., et al., *Deletion of a Conserved cis-Element in the Ifng Locus Highlights the Role of Acute Histone Acetylation in Modulating Inducible Gene Transcription*. Plos Genetics, 2014. **10**(1).
305. Balasubramani, A., et al., *Deletion of a Conserved cis-Element in the Ifng Locus Highlights the Role of Acute Histone Acetylation in Modulating Inducible Gene Transcription*. Plos Genetics, 2014. **10**(1).
306. Bargiela, A., et al., *Two Enhancers Control Transcription of Drosophila muscleblind in the Embryonic Somatic Musculature and in the Central Nervous System*. Plos One, 2014. **9**(3).
307. Barnhill, L.M., et al., *High Expression of CAI2, a 9p21-Embedded Long Noncoding RNA, Contributes to Advanced-Stage Neuroblastoma*. Cancer Research, 2014. **74**(14): p. 3753-3763.
308. Barriere, A. and I. Ruvinsky, *Pervasive Divergence of Transcriptional Gene Regulation in Caenorhabditis Nematodes*. Plos Genetics, 2014. **10**(6).
309. Bazil, J.N., et al., *The Inferred Cardiogenic Gene Regulatory Network in the Mammalian Heart*. Plos One, 2014. **9**(6).
310. Bhatia, S., et al., *A survey of ancient conserved non-coding elements in the PAX6 locus reveals a landscape of interdigitated cis-regulatory archipelagos*. Developmental Biology, 2014. **387**(2): p. 214-228.
311. Bielsa, B., et al., *Detection of SNP and validation of a SFP InDel (deletion) in inverted repeat region of the Prunus species chloroplast genome*. Scientia Horticulturae, 2014. **168**: p. 108-112.
312. Boden, S.A., et al., *EARLY FLOWERING3 Regulates Flowering in Spring Barley by Mediating Gibberellin Production and FLOWERING LOCUS T Expression*. Plant Cell, 2014. **26**(4): p. 1557-1569.
313. Boyer-Di Ponio, J., et al., *Instruction of Circulating Endothelial Progenitors In Vitro towards Specialized Blood-Brain Barrier and Arterial Phenotypes*. Plos One, 2014. **9**(1).
314. Braasch, I., et al., *Connectivity of vertebrate genomes: Paired-related homeobox (Prrx) genes in spotted gar, basal teleosts, and tetrapods*. Comparative Biochemistry and Physiology C-Toxicology & Pharmacology, 2014. **163**: p. 24-36.
315. Breton, C.M., et al., *The self-incompatibility mating system of the olive (*Olea**

- europaea L.) functions with dominance between S-alleles.* Tree Genetics & Genomes, 2014. **10**(4): p. 1055-1067.
- 316. Butts, T., et al., *The evolution of the vertebrate cerebellum: absence of a proliferative external granule layer in a non-teleost ray-finned fish.* Evolution & Development, 2014. **16**(2): p. 92-100.
  - 317. Cai, Q., et al., *Jasmonic acid regulates spikelet development in rice.* Nature Communications, 2014. **5**.
  - 318. Campoli, C. and M. von Korff, *Genetic Control of Reproductive Development in Temperate Cereals,* in *Molecular Genetics of Floral Transition and Flower Development*, F. Fornara, Editor. 2014. p. 131-158.
  - 319. Capella, M., et al., *Plant homeodomain-leucine zipper I transcription factors exhibit different functional AHA motifs that selectively interact with TBP or/and TFIIIB.* Plant Cell Reports, 2014. **33**(6): p. 955-967.
  - 320. Castric, V., S. Billiard, and X. Vekemans, *Trait Transitions in Explicit Ecological and Genomic Contexts: Plant Mating Systems as Case Studies,* in *Ecological Genomics: Ecology and the Evolution of Genes and Genomes*, C.R. Landry and N. AubinHorth, Editors. 2014. p. 7-36.
  - 321. Cerqueira, G.C., et al., *The Aspergillus Genome Database: multispecies curation and incorporation of RNA-Seq data to improve structural gene annotations.* Nucleic Acids Research, 2014. **42**(D1): p. D705-D710.
  - 322. Cerrato, F., A. De Crescenzo, and A. Riccio, *Looking for CDKN1C enhancers.* European Journal of Human Genetics, 2014. **22**(4): p. 442-443.
  - 323. Chaumont, F. and S.D. Tyerman, *Aquaporins: Highly Regulated Channels Controlling Plant Water Relations.* Plant Physiology, 2014. **164**(4): p. 1600-1618.
  - 324. Chen, S., et al., *Whole-genome sequence of a flatfish provides insights into ZW sex chromosome evolution and adaptation to a benthic lifestyle.* Nature Genetics, 2014. **46**(3): p. 253-+.
  - 325. Chen, W.-C., et al., *Dissection of a Ciona regulatory element reveals complexity of cross-species enhancer activity.* Developmental Biology, 2014. **390**(2): p. 261-272.
  - 326. Chew, Y.H., et al., *Mathematical Models Light Up Plant Signaling.* Plant Cell, 2014. **26**(1): p. 5-20.
  - 327. Chow, B.Y., et al., *Transcriptional Regulation of LUX by CBF1 Mediates Cold Input to the Circadian Clock in Arabidopsis.* Current Biology, 2014. **24**(13): p. 1518-1524.
  - 328. Coelho, A., et al., *Genetic variation in CD36, HBA, NOS3 and VCAM1 is associated with chronic haemolysis level in sickle cell anaemia: a longitudinal study.* European Journal of Haematology, 2014. **92**(3): p. 237-243.
  - 329. Cortez, D., et al., *Origins and functional evolution of Y chromosomes across mammals.* Nature, 2014. **508**(7497): p. 488-+.
  - 330. Cota, C.D., F. Segade, and B. Davidson, *Heart genetics in a small package, exploiting the condensed genome of Ciona intestinalis.* Briefings in Functional Genomics, 2014. **13**(1): p. 3-14.
  - 331. Cui, X.-P., et al., *HOXA10 Promotes Cell Invasion and MMP-3 Expression Via TGF beta 2-Mediated Activation of the p38 MAPK Pathway in Pancreatic Cancer Cells.* Digestive Diseases and Sciences, 2014. **59**(7): p. 1442-1451.

332. Cui, Z., Q. Xu, and X. Wang, *Regulation of the circadian clock through pre-mRNA splicing in Arabidopsis*. Journal of Experimental Botany, 2014. **65**(8): p. 1973-1980.
333. Dai, Z., Y. Xiong, and X. Dai, *The Pattern and Evolution of Looped Gene Bendability*. Molecular Biology and Evolution, 2014. **31**(2): p. 319-329.
334. Daido, Y., S. Hamanishi, and T.G. Kusakabe, *Transcriptional co-regulation of evolutionarily conserved microRNA/cone opsin gene pairs: Implications for photoreceptor subtype specification*. Developmental Biology, 2014. **392**(1): p. 117-129.
335. de Lucas, M. and S. Prat, *PIFs get BRright: PHYTOCHROME INTERACTING FACTORs as integrators of light and hormonal signals*. New Phytologist, 2014. **202**(4): p. 1126-1141.
336. Della Pina, S., E. Souer, and R. Koes, *Arguments in the evo-devo debate: say it with flowers!* Journal of Experimental Botany, 2014. **65**(9): p. 2231-2242.
337. Dreni, L. and M.M. Kater, *MADS reloaded: evolution of the AGAMOUS subfamily genes*. New Phytologist, 2014. **201**(3): p. 717-732.
338. Evans, D.S., et al., *Genetic Association Study of Adiposity and Melanocortin-4 Receptor (MC4R) Common Variants: Replication and Functional Characterization of Non-Coding Regions*. Plos One, 2014. **9**(5).
339. Favorova, O.O., et al., *Genome-wide association study as a method to analyze the genome architecture in polygenic diseases, with the example of multiple sclerosis*. Molecular Biology, 2014. **48**(4): p. 496-507.
340. Ferg, M., et al., *Gene transcription in the zebrafish embryo: regulators and networks*. Briefings in Functional Genomics, 2014. **13**(2): p. 131-143.
341. Fogelmark, K. and C. Troein, *Rethinking Transcriptional Activation in the Arabidopsis Circadian Clock*. Plos Computational Biology, 2014. **10**(7).
342. Fu, J., L. Yang, and S. Dai, *Conservation of Arabidopsis thaliana circadian clock genes in Chrysanthemum lavandulifolium*. Plant Physiology and Biochemistry, 2014. **80**: p. 337-347.
343. Fujimoto, T., et al., *A Novel Complex Recombinant Form of Type 48-Related Human Adenovirus Species D Isolated in Japan*. Japanese Journal of Infectious Diseases, 2014. **67**(4): p. 282-287.
344. Furutani, M., Y. Nakano, and M. Tasaka, *MAB4-induced auxin sink generates local auxin gradients in Arabidopsis organ formation*. Proceedings of the National Academy of Sciences of the United States of America, 2014. **111**(3): p. 1198-1203.
345. Gallagher, J.E.G., et al., *Divergence in a master variator generates distinct phenotypes and transcriptional responses*. Genes & Development, 2014. **28**(4): p. 409-421.
346. Garg, A., et al., *KLHL40 deficiency destabilizes thin filament proteins and promotes nemaline myopathy*. Journal of Clinical Investigation, 2014. **124**(8): p. 3529-3539.
347. Gonzalez, G., et al., *Intertypic modular exchanges of genomic segments by homologous recombination at universally conserved segments in human adenovirus species D*. Gene, 2014. **547**(1): p. 10-17.
348. Grigoriev, I.V., et al., *MycoCosm portal: gearing up for 1000 fungal genomes*.

- Nucleic Acids Research, 2014. **42**(D1): p. D699-D704.
349. Guenther, C.A., et al., *A molecular basis for classic blond hair color in Europeans*. Nature Genetics, 2014. **46**(7): p. 748-752.
350. Gyllenstrand, N., et al., *No Time for Spruce: Rapid Dampening of Circadian Rhythms in Picea abies (L. Karst)*. Plant and Cell Physiology, 2014. **55**(3): p. 535-550.
351. Hao, H., et al., *Identification of a transient Sox5 expressing progenitor population in the neonatal ventral forebrain by a novel cis-regulatory element*. Developmental Biology, 2014. **393**(1): p. 183-193.
352. Haro, E., et al., *Sp6 and Sp8 Transcription Factors Control AER Formation and Dorsal-Ventral Patterning in Limb Development*. Plos Genetics, 2014. **10**(8).
353. Heule, C., W. Salzburger, and A. Boehne, *Genetics of Sexual Development: An Evolutionary Playground for Fish*. Genetics, 2014. **196**(3): p. 579-591.
354. Hodar, C., et al., *Comparative gene expression analysis of Dtg, a novel target gene of Dpp signaling pathway in the early Drosophila melanogaster embryo*. Gene, 2014. **535**(2): p. 210-217.
355. Holt, A.L., et al., *Signaling in shoot and flower meristems of Arabidopsis thaliana*. Current Opinion in Plant Biology, 2014. **17**: p. 96-102.
356. Hong, C.-S., et al., *Transcription Factor AP2 Epsilon (Tfap2e) Regulates Neural Crest Specification in Xenopus*. Developmental Neurobiology, 2014. **74**(9): p. 894-906.
357. Horstman, A., et al., *AINTEGUMENTA-LIKE proteins: hubs in a plethora of networks*. Trends in Plant Science, 2014. **19**(3): p. 146-157.
358. Hsu, P.Y. and S.L. Harmer, *Wheels within wheels: the plant circadian system*. Trends in Plant Science, 2014. **19**(4): p. 240-249.
359. Hu, S., et al., *Molecular characterization, tissue distribution, and expression of two ovarian Dicer isoforms during follicle development in goose (Anser cygnoides)*. Comparative Biochemistry and Physiology B-Biochemistry & Molecular Biology, 2014. **170**: p. 33-41.
360. Hua, L.L., et al., *Specification of the mouse cardiac conduction system in the absence of Endothelin signaling*. Developmental Biology, 2014. **393**(2): p. 245-254.
361. Huang, H., et al., *Thirteen Camellia chloroplast genome sequences determined by high-throughput sequencing: genome structure and phylogenetic relationships*. Bmc Evolutionary Biology, 2014. **14**.
362. Huang, W., et al., *Natural variation in genome architecture among 205 Drosophila melanogaster Genetic Reference Panel lines*. Genome Research, 2014. **24**(7): p. 1193-1208.
363. Iglesias-Fernandez, R., et al., *The AtCathB3 gene, encoding a cathepsin B-like protease, is expressed during germination of Arabidopsis thaliana and transcriptionally repressed by the basic leucine zipper protein GBF1*. Journal of Experimental Botany, 2014. **65**(8): p. 2009-2021.
364. Johansson, M., et al., *The Perennial Clock Is an Essential Timer for Seasonal Growth Events and Cold Hardiness*, in *Plant Circadian Networks: Methods and Protocols*, D. Staiger, Editor. 2014. p. 297-311.
365. Johnson, A.L., R. Govindarajulu, and T.-L. Ashman, *Bioclimatic evaluation of*

*geographical range in Fragaria (Rosaceae): consequences of variation in breeding system, ploidy and species age.* Botanical Journal of the Linnean Society, 2014. **176**(1): p. 99-114.

366. Kawakami-Schulz, S.V., et al., *Serum response factor: positive and negative regulation of an epithelial gene expression network in the destrin mutant cornea.* Physiological Genomics, 2014. **46**(8): p. 277-289.
367. Kim, H.T., M.G. Chung, and K.-J. Kim, *Chloroplast Genome Evolution in Early Diverged Leptosporangiate Ferns.* Molecules and Cells, 2014. **37**(5): p. 372-382.
368. Kim, H.T. and K.-J. Kim, *Chloroplast Genome Differences between Asian and American Equisetum arvense (Equisetaceae) and the Origin of the Hypervariable trnY-trnE Intergenic Spacer.* Plos One, 2014. **9**(8).
369. Kipanyula, M.J., et al., *Signaling pathways bridging fate determination of neural crest cells to glial lineages in the developing peripheral nervous system.* Cellular Signalling, 2014. **26**(4): p. 673-682.
370. Kitashiba, H. and J.B. Nasrallah, *Self-incompatibility in Brassicaceae crops: lessons for interspecific incompatibility.* Breeding Science, 2014. **64**(1): p. 23-37.
371. Kornman, K.S. and P.J. Polverini, *Clinical application of genetics to guide prevention and treatment of oral diseases.* Clinical Genetics, 2014. **86**(1): p. 44-49.
372. Kumagai, K., et al., *Observation of Glycolytic Metabolites in Tumor Cell Lysate by Using Hyperpolarization of Deuterated Glucose.* Biological & Pharmaceutical Bulletin, 2014. **37**(8): p. 1416-1421.
373. Kumar, V., et al., *Comparative transcriptome analysis of ovules reveals stress related genes associated with nucellar polyembryony in citrus.* Tree Genetics & Genomes, 2014. **10**(3): p. 449-464.
374. Leducq, J.-B., et al., *Self-Incompatibility in Brassicaceae: Identification and Characterization of SRK-Like Sequences Linked to the S-Locus in the Tribe Biscutelleae.* G3-Genes Genomes Genetics, 2014. **4**(6): p. 983-992.
375. Lee, J., et al., *Combined Analysis of the Chloroplast Genome and Transcriptome of the Antarctic Vascular Plant Deschampsia antarctica Desv.* Plos One, 2014. **9**(3).
376. Leivar, P. and E. Monte, *PIFs: Systems Integrators in Plant Development.* Plant Cell, 2014. **26**(1): p. 56-78.
377. Li, Q., et al., *miR-224 promotion of cell migration and invasion by targeting Homeobox D 10 gene in human hepatocellular carcinoma.* Journal of Gastroenterology and Hepatology, 2014. **29**(4): p. 835-842.
378. Li, R., et al., *Isl1 and Pou4f2 Form a Complex to Regulate Target Genes in Developing Retinal Ganglion Cells.* Plos One, 2014. **9**(3).
379. Liew, L.C., et al., *The Pea Photoperiod Response Gene STERILE NODES Is an Ortholog of LUX ARRHYTHMO.* Plant Physiology, 2014. **165**(2): p. 648-657.
380. Liu, Y., et al., *Hhex and Cer1 Mediate the Sox17 Pathway for Cardiac Mesoderm Formation in Embryonic Stem Cells.* Stem Cells, 2014. **32**(6): p. 1515-1526.
381. Luo, J., et al., *Comparative Chloroplast Genomes of Photosynthetic Orchids: Insights into Evolution of the Orchidaceae and Development of Molecular Markers for Phylogenetic Applications.* Plos One, 2014. **9**(6).
382. Lynch, D.C., et al., *Disrupted auto-regulation of the spliceosomal gene SNRPB*

- causes cerebro-costo-mandibular syndrome.* Nature Communications, 2014. **5**.
383. Manousaki, T., et al., *The sex-specific transcriptome of the hermaphrodite sparid sharpsnout seabream (Diplodus puntazzo).* Bmc Genomics, 2014. **15**.
384. Matilla, M.A. and G.P.C. Salmond, *Bacteriophage phi MAM1, a Viunalikevirus, Is a Broad-Host-Range, High-Efficiency Generalized Transducer That Infects Environmental and Clinical Isolates of the Enterobacterial Genera Serratia and Kluyvera.* Applied and Environmental Microbiology, 2014. **80**(20): p. 6446-6457.
385. Mazaud-Guittot, S., et al., *GATA4 Autoregulates Its Own Expression in Mouse Gonadal Cells via Its Distal 1b Promoter.* Biology of Reproduction, 2014. **90**(2).
386. Meier, S., et al., *Hyperpolarized NMR Probes for Biological Assays.* Sensors, 2014. **14**(1): p. 1576-1597.
387. Milton, J.N. and G.J. Kato, *Genetic determinants of haemolysis in sickle cell anaemia (vol 161, pg 270, 2013).* British Journal of Haematology, 2014. **166**(3): p. 468-468.
388. Mizzotti, C., B.M. Galliani, and S. Masiero, *The backstage of the ABC model: The Antirrhinum majus contribution.* Plant Biosystems, 2014. **148**(1): p. 176-186.
389. Monteiro, A.S., R. Freitas, and I. Palmeirim, *Genomics of zebrafish hoxba and hoxbb loci.* Journal of Applied Ichthyology, 2014. **30**(4): p. 689-695.
390. Mueller, L.M., M. von Korff, and S.J. Davis, *Connections between circadian clocks and carbon metabolism reveal species-specific effects on growth control.* Journal of Experimental Botany, 2014. **65**(11): p. 2915-2923.
391. Muino, J.M., et al., *Structural determinants of DNA recognition by plant MADS-domain transcription factors.* Nucleic Acids Research, 2014. **42**(4): p. 2138-2146.
392. Mulley, J.F. and P.W.H. Holland, *Genomic organisation of the seven ParaHox genes of coelacanths.* Journal of Experimental Zoology Part B-Molecular and Developmental Evolution, 2014. **322**(6): p. 352-358.
393. Myburg, A.A., et al., *The genome of Eucalyptus grandis.* Nature, 2014. **510**(7505): p. 356-+.
394. Nam, J.H., et al., *Genomic stability of adipogenic human adenovirus 36.* International Journal of Obesity, 2014. **38**(2): p. 321-324.
395. O'Connor, C.M., et al., *A comparative study of an innate immune response in Lamprologine cichlid fishes.* Naturwissenschaften, 2014. **101**(10): p. 839-849.
396. O'Maoileidigh, D.S., E. Graciet, and F. Wellmer, *Genetic Control of Arabidopsis Flower Development, in Molecular Genetics of Floral Transition and Flower Development,* F. Fornara, Editor. 2014. p. 159-190.
397. O'Maoileidigh, D.S., E. Graciet, and F. Wellmer, *Gene networks controlling Arabidopsis thaliana flower development.* New Phytologist, 2014. **201**(1): p. 16-30.
398. Park, S., et al., *Conserved regulation of hoxc11 by pitx1 in Anolis lizards.* Journal of Experimental Zoology Part B-Molecular and Developmental Evolution, 2014. **322**(3): p. 156-165.
399. Pauly, M., et al., *High prevalence and diversity of species D adenoviruses (HAdV-D) in human populations of four Sub-Saharan countries.* Virology Journal, 2014. **11**.
400. Pecon-Slattery, J., *Recent Advances in Primate Phylogenomics.* Annual Review of Animal Biosciences, Vol 2, 2014. **2**: p. 41-63.

401. Polimanti, R., et al., *In silico analysis of TTR gene (coding and non-coding regions, and interactive network) and its implications in transthyretin-related amyloidosis*. Amyloid-Journal of Protein Folding Disorders, 2014. **21**(3): p. 154-162.
402. Polychronopoulos, D., D. Sellis, and Y. Almirantis, *Conserved Noncoding Elements Follow Power-Law-Like Distributions in Several Genomes as a Result of Genome Dynamics*. Plos One, 2014. **9**(5).
403. Prashar, P., et al., *Microarray meta-analysis identifies evolutionarily conserved BMP signaling targets in developing long bones*. Developmental Biology, 2014. **389**(2): p. 192-207.
404. Ravi, P., et al., *Small-scale transcriptomics reveals differences among gonadal stages in Asian seabass (*Lates calcarifer*)*. Reproductive Biology and Endocrinology, 2014. **12**.
405. Rebolledo-Jaramillo, B., et al., *Cis-regulatory elements are harbored in Intron5 of the RUNX1 gene*. Bmc Genomics, 2014. **15**.
406. Ricardi, M.M., et al., *Genome-wide data ( ChIP-seq) enabled identification of cell wall-related and aquaporin genes as targets of tomato ASR1, a drought stress-responsive transcription factor*. Bmc Plant Biology, 2014. **14**.
407. Roeland Boer, D., et al., *Structural Basis for DNA Binding Specificity by the Auxin-Dependent ARF Transcription Factors*. Cell, 2014. **156**(3): p. 577-589.
408. Rothchild, A.C., et al., *iNKT Cell Production of GM- CSF Controls Mycobacterium tuberculosis*. Plos Pathogens, 2014. **10**(1).
409. Roure, A., P. Lemaire, and S. Darras, *An Otx/Nodal Regulatory Signature for Posterior Neural Development in Ascidians*. Plos Genetics, 2014. **10**(8).
410. Saha, N.R., et al., *Genome complexity in the coelacanth is reflected in its adaptive immune system*. Journal of Experimental Zoology Part B-Molecular and Developmental Evolution, 2014. **322**(6): p. 438-463.
411. Salio, M., et al., *Biology of CD1-and MR1-Restricted T Cells*. Annual Review of Immunology, Vol 32, 2014. **32**: p. 323-366.
412. Sanchez-Ferras, O., et al., *Induction and dorsal restriction of Paired-box 3 (Pax3) gene expression in the caudal neuroectoderm is mediated by integration of multiple pathways on a short neural crest enhancer*. Biochimica Et Biophysica Acta-Gene Regulatory Mechanisms, 2014. **1839**(7): p. 546-558.
413. Seo, P.J. and P. Mas, *Multiple Layers of Posttranslational Regulation Refine Circadian Clock Activity in Arabidopsis*. Plant Cell, 2014. **26**(1): p. 79-87.
414. Serrano-Candelas, E., et al., *The Vertebrate RCAN Gene Family: Novel Insights into Evolution, Structure and Regulation*. Plos One, 2014. **9**(1).
415. Serrat, R., et al., *The Armc10/SVH gene: genome context, regulation of mitochondrial dynamics and protection against A beta-induced mitochondrial fragmentation*. Cell Death & Disease, 2014. **5**.
416. Shi, F., et al., *A piggyBac insertion disrupts Foxl2 expression that mimics BPES syndrome in mice*. Human Molecular Genetics, 2014. **23**(14): p. 3792-3800.
417. Shi, X., et al., *Cooperative interaction of Etv2 and Gata2 regulates the development of endothelial and hematopoietic lineages*. Developmental Biology, 2014. **389**(2): p. 208-218.
418. So, J.-S., et al., *6-Methoxyflavone Inhibits NFAT Translocation into the Nucleus*

- and Suppresses T Cell Activation.* Journal of Immunology, 2014. **193**(6): p. 2772-2783.
419. Soltis, D.E., et al., *Are polyploids really evolutionary dead-ends ( again)? A critical reappraisal of Mayrose et al. (2011).* New Phytologist, 2014. **202**(4): p. 1105-1117.
420. Song, C.-g., et al., *The effect of procyanidin on expression of STAT1 in type 2 diabetes mellitus SD rats with focal cerebral ischemia.* Neuroendocrinology Letters, 2014. **35**(1): p. 68-72.
421. Song, X., et al., *Genes associated with agronomic traits in non-heading Chinese cabbage identified by expression profiling.* Bmc Plant Biology, 2014. **14**.
422. Soulavie, F., et al., *hemingway is required for sperm flagella assembly and ciliary motility in Drosophila.* Molecular Biology of the Cell, 2014. **25**(8): p. 1276-1286.
423. Stolfi, A., et al., *Divergent mechanisms regulate conserved cardiopharyngeal development and gene expression in distantly related ascidians.* Elife, 2014. **3**.
424. Stowell, K.M., *DNA Testing for Malignant Hyperthermia: The Reality and the Dream.* Anesthesia and Analgesia, 2014. **118**(2): p. 397-406.
425. Su, Y.-C., et al., *Comparative genomic analysis reveals distinct genotypic features of the emerging pathogen Haemophilus influenzae type f.* Bmc Genomics, 2014. **15**.
426. Sulakhe, D., et al., *High-Throughput Translational Medicine: Challenges and Solutions, in Systems Analysis of Human Multigene Disorders,* N. Maltsev, A. Rzhetsky, and T.C. Gilliam, Editors. 2014. p. 39-67.
427. Teo, Z.W.N., et al., *New insights into the regulation of inflorescence architecture.* Trends in Plant Science, 2014. **19**(3): p. 158-165.
428. Terakami, S., et al., *Transcriptome-based single nucleotide polymorphism markers for genome mapping in Japanese pear (*Pyrus pyrifolia Nakai*).* Tree Genetics & Genomes, 2014. **10**(4): p. 853-863.
429. van Dijk, T., et al., *Genomic rearrangements and signatures of breeding in the allo-octoploid strawberry as revealed through an allele dose based SSR linkage map.* Bmc Plant Biology, 2014. **14**.
430. Vausort, M., D.R. Wagner, and Y. Devaux, *Long Noncoding RNAs in Patients With Acute Myocardial Infarction.* Circulation Research, 2014. **115**(7): p. 668-U180.
431. Vekemans, X., et al., *The evolution of selfing from outcrossing ancestors in Brassicaceae: what have we learned from variation at the S-locus?* Journal of Evolutionary Biology, 2014. **27**(7): p. 1372-1385.
432. Vercruyssen, L., et al., *ANGUSTIFOLIA3 Binds to SWI/SNF Chromatin Remodeling Complexes to Regulate Transcription during Arabidopsis Leaf Development.* Plant Cell, 2014. **26**(1): p. 210-229.
433. Verkest, A., et al., *A Generic Tool for Transcription Factor Target Gene Discovery in Arabidopsis Cell Suspension Cultures Based on TandemChromatinAffinity Purification.* Plant Physiology, 2014. **164**(3): p. 1122-1133.
434. Vieira, L.d.N., et al., *The Complete Chloroplast Genome Sequence of *Podocarpus lambertii*: Genome Structure, Evolutionary Aspects, Gene Content and SSR Detection.* Plos One, 2014. **9**(3).
435. Walker, J.F., M.J. Zanis, and N.C. Emery, *COMPARATIVE ANALYSIS OF*

*COMPLETE CHLOROPLAST GENOME SEQUENCE AND INVERSION VARIATION IN LASTHENIA BURKEI (MADIEAE, ASTERACEAE)*. American Journal of Botany, 2014. **101**(4): p. 722-729.

436. Wang, L., et al., *Genome sequencing of the high oil crop sesame provides insight into oil biosynthesis*. Genome Biology, 2014. **15**(2).
437. Wang, Q.f., et al., *Regulation of MEIS1 by distal enhancer elements in acute leukemia*. Leukemia, 2014. **28**(1): p. 138-146.
438. Wang, X., H. Guo, and J. Wang, *Insights into the Common Ancestor of Cereals*, in *Genomes of Herbaceous Land Plants*, A.H. Paterson, Editor. 2014. p. 175-194.
439. Wang, Y., et al., *The Stem Cell Niche in Leaf Axils Is Established by Auxin and Cytokinin in Arabidopsis*. Plant Cell, 2014. **26**(5): p. 2055-2067.
440. Wellmer, F., E. Graciet, and J. Luis Riechmann, *Specification of floral organs in Arabidopsis*. Journal of Experimental Botany, 2014. **65**(1): p. 1-9.
441. Wencker, M., et al., *Innate-like T cells straddle innate and adaptive immunity by altering antigen-receptor responsiveness*. Nature Immunology, 2014. **15**(1): p. 80-87.
442. Wessels, J.M., et al., *The Brain-Uterus Connection: Brain Derived Neurotrophic Factor (BDNF) and Its Receptor (Ntrk2) Are Conserved in the Mammalian Uterus*. Plos One, 2014. **9**(4).
443. Wu, C.-L., et al., *NF- $\kappa$ B but not FoxO sites in the MuRF1 promoter are required for transcriptional activation in disuse muscle atrophy*. American Journal of Physiology-Cell Physiology, 2014. **306**(8): p. C762-C767.
444. Xie, Q., et al., *LNK1 and LNK2 Are Transcriptional Coactivators in the Arabidopsis Circadian Oscillator*. Plant Cell, 2014. **26**(7): p. 2843-2857.
445. Yaguchi, K., et al., *Identification of transcriptional regulatory elements for Ntnng1 and Ntnng2 genes in mice*. Molecular Brain, 2014. **7**.
446. Yang, J.-B., D.-Z. Li, and H.-T. Li, *Highly effective sequencing whole chloroplast genomes of angiosperms by nine novel universal primer pairs*. Molecular Ecology Resources, 2014. **14**(5): p. 1024-1031.
447. Yoshikawa, T., et al., *Epistatic effects of multiple receptor genes on pathophysiology of asthma - its limits and potential for clinical application*. Medical Science Monitor, 2014. **20**: p. 64-71.
448. Young, J.J., et al., *Spalt-like 4 promotes posterior neural fates via repression of pou5f3 family members in Xenopus*. Development, 2014. **141**(8): p. 1683-1693.
449. Zhalnina, K.V., et al., *Genome Sequence of Candidatus Nitrososphaera evergladensis from Group I.1b Enriched from Everglades Soil Reveals Novel Genomic Features of the Ammonia-Oxidizing Archaea*. Plos One, 2014. **9**(7).
450. Zhang, E.-b., et al., *Long noncoding RNA ANRIL indicates a poor prognosis of gastric cancer and promotes tumor growth by epigenetically silencing of miR-99a/miR-449a*. Oncotarget, 2014. **5**(8): p. 2276-2292.
451. Zhang, J.-Y., et al., *Auxin inhibits stomatal development through MONOPTEROS repression of a mobile peptide gene STOMAGEN in mesophyll*. Proceedings of the National Academy of Sciences of the United States of America, 2014. **111**(29): p. E3015-E3023.
452. Zhang, X.-O., et al., *Species-specific alternative splicing leads to unique expression of sno-lncRNAs*. Bmc Genomics, 2014. **15**.

453. Zhang, Y., et al., *Complete chloroplast genome sequences of Praxelis (Eupatorium catarium Veldkamp), an important invasive species*. Gene, 2014. **549**(1): p. 58-69.
454. Zhou, C., et al., *The genome sequence of a novel simian adenovirus in a chimpanzee reveals a close relationship to human adenoviruses*. Archives of Virology, 2014. **159**(7): p. 1765-1770.